RAW SEQUENCE LISTING

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Application Serial Number: _____ 10/642,272 A

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PATENT APPLICATION: US/10/642,272A TIME: 17:51:16

Input Set : A:\10642272.ST25.txt
Output Set: N:\CRF4\08292005\J642272A.raw

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 3 <110> APPLICANT: Hattori, Fumiyuki
 4        Sugimura, Keijiro
 5        Furuya, Mayumi
 7 <120> TITLE OF INVENTION: Therapeutic Methods and Agents for Diseases Associated with
 8        Decreased Expression of AOP-1 Gene or AOP-1
10 <130> FILE REFERENCE: 58777.000012
12 <140> CURRENT APPLICATION NUMBER: 10/642,272A
13 <141> CURRENT FILING DATE: 2003-08-18
15 <150> PRIOR APPLICATION NUMBER: PCT/JP02/01358
16 <151> PRIOR FILING DATE: 2001-02-18
18 <150> PRIOR APPLICATION NUMBER: JP 41003/2001
19 <151> PRIOR FILING DATE: 2001-02-16
21 <160> NUMBER OF SEQ ID NOS: 30
23 <170> SOFTWARE: PatentIn version 3.3
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26 <211> LENGTH: 1542
27 <212> TYPE: DNA
28 <213> ORGANISM: Homo sapiens
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35 agcttgacaa atttattgtg ttctggttcc agtcaagcaa aattattcag caccagttcc   180
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51 agcgtcaacg atctcccagt gggccgaagc gtggaagaaa ccctccgctt ggtgaaggcg   660
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63 ctagtacagg aatcgtttat tggtaacatc ttggtggctg gctagctagt ttctacagaa  1020
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67 tcttagcctt acttgaatct tgcctataat aaagtagagc aacacacatt gaaagcttct  1140
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 98 ccattttaaa ggtactgctg ttgtcaatgg agagttcaaa gagctgagtc tcgacgactt    300
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130 agtgaaagct tctgatcaag gtcctgaaat ttcctcttgg atttttgtta attatgctga   1260
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142 <213> ORGANISM: Mus sp.
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149 ctgcctcaac agttcttagg cctgttgctt ctagaagaac ctgtttgaca gacatactgt    180
151 ggtctgcctc tgcccaagga aagtcagcct ttagcaccag ttcctctttc cacacccctg    240
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157 tcacatttgt gtgtcctaca gaaattgttg ctttcagtga caaagccaat gaatttcatg    420
159 atgtaaactg tgaagtagtt gcagtttcag tggattccca cttcagtcat cttgcctgga    480
161 tcaacacacc aagaaagaat ggtggtttgg ccacatgaa catcacactg ttgtcggata     540
163 taactaagca gatatcccga gactacggag tgctgttgga aagtgctggc attgcactca    600
165 gaggtctctt cattattgac cctaatggtg tcgtcaagca cctgagtgtc aacgaccttc    660
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196 <212> TYPE: PRT
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199 <400> SEQUENCE: 4
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205 Val Ser Ala Ile Pro Trp Gly Ile Ser Ala Thr Ala Ala Leu Arg Pro
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209 Ala Ala Cys Gly Arg Thr Ser Leu Thr Asn Leu Leu Cys Ser Gly Ser
210         35                  40                  45
213 Ser Gln Ala Lys Leu Phe Ser Thr Ser Ser Ser Cys His Ala Pro Ala
214     50                  55                  60
217 Val Thr Gln His Ala Pro Tyr Phe Lys Gly Thr Ala Val Val Asn Gly
218 65                  70                  75                  80
221 Glu Phe Lys Asp Leu Ser Leu Asp Asp Phe Lys Gly Lys Tyr Leu Val
222             85                  90                  95
225 Leu Phe Phe Tyr Pro Leu Asp Phe Thr Phe Val Cys Pro Thr Glu Ile
226             100                 105                 110
229 Val Ala Phe Ser Asp Lys Ala Asn Glu Phe His Asp Val Asn Cys Glu
230         115                 120                 125
233 Val Val Ala Val Ser Val Asp Ser His Phe Ser His Leu Ala Trp Ile
234     130                 135                 140
237 Asn Thr Pro Arg Lys Asn Gly Gly Leu Gly His Met Asn Ile Ala Leu
238 145                 150                 155                 160
241 Leu Ser Asp Leu Thr Lys Gln Ile Ser Arg Asp Tyr Gly Val Leu Leu
242             165                 170                 175
245 Glu Gly Ser Gly Leu Ala Leu Arg Gly Leu Phe Ile Ile Asp Pro Asn
246             180                 185                 190
249 Gly Val Ile Lys His Leu Ser Val Asn Asp Leu Pro Val Gly Arg Ser
250         195                 200                 205
253 Val Glu Glu Thr Leu Arg Leu Val Lys Ala Phe Gln Tyr Val Glu Thr
254     210                 215                 220
257 His Gly Glu Val Cys Pro Ala Asn Trp Thr Pro Asp Ser Pro Thr Ile
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280 Val Ala Ser Arg Arg Thr Cys Leu Thr Asp Met Leu Trp Ser Ala Cys
281         35                  40                  45
284 Pro Gln Ala Lys Phe Ala Phe Ser Thr Ser Ser Ser Phe His Thr Pro
285     50                  55                  60
288 Ala Val Thr Gln His Ala Pro His Phe Lys Gly Thr Ala Val Val Asn
289 65                  70                  75                  80
292 Gly Glu Phe Lys Glu Leu Ser Leu Asp Asp Phe Lys Gly Lys Tyr Leu
293                 85                  90                  95
296 Val Leu Phe Phe Tyr Pro Leu Asp Phe Thr Phe Val Cys Pro Thr Glu
297             100                 105                 110
300 Ile Val Ala Phe Ser Asp Lys Ala Asn Glu Phe His Asp Val Asn Cys
301         115                 120                 125
304 Glu Val Val Ala Val Ser Val Asp Ser His Phe Ser His Leu Ala Trp
305     130                 135                 140
308 Ile Asn Thr Pro Ala Lys Asn Gly Gly Leu Gly His Met Asn Ile Thr
309 145                 150                 155                 160
312 Leu Leu Ser Asp Leu Thr Lys Gln Ile Ser Arg Asp Tyr Gly Val Leu
313                 165                 170                 175
316 Leu Glu Ser Ala Gly Ile Ala Leu Arg Gly Leu Phe Ile Ile Asp Pro
317             180                 185                 190
320 Asn Gly Val Ile Lys His Leu Ser Val Asn Asp Leu Pro Val Gly Arg
321             195                 200                 205
324 Ser Val Glu Glu Pro Leu Arg Leu Val Lys Ala Phe Gln Phe Val Glu
325     210                 215                 220
328 Thr His Gly Glu Val Cys Pro Pro Asn Trp Thr Pro Glu Ser Pro Thr
329 225                 230                 235                 240
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333             245                 250                 255
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341 <211> LENGTH: 257
342 <212> TYPE: PRT
343 <213> ORGANISM: Mus sp.
345 <400> SEQUENCE: 6
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351 Ala Ser Ala Ile Ser Arg Ser Ile Ser Ala Ser Thr Val Leu Arg Pro
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355 Val Ala Ser Arg Arg Thr Cys Leu Thr Asp Ile Leu Trp Ser Ala Ser
356         35                  40                  45
359 Ala Gln Gly Leu Ser Ala Phe Ser Thr Ser Ser Ser Phe His Thr Pro
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367 Gly Glu Phe Lys Glu Leu Ser Leu Asp Asp Phe Lys Gly Lys Tyr Leu
368                     85                      90                      95
371 Val Leu Phe Phe Tyr Pro Leu Asp Phe Thr Phe Val Cys Pro Thr Glu
372                     100                     105                     110
375 Ile Val Ala Phe Ser Asp Lys Ala Asn Glu Phe His Asp Val Asn Cys
376             115                     120                     125
379 Glu Val Val Ala Val Ser Val Asp Ser His Phe Ser His Leu Ala Trp
380         130                     135                     140
383 Ile Asn Thr Pro Arg Lys Asn Gly Gly Leu Gly His Met Asn Ile Thr
384 145                     150                     155                     160
387 Leu Leu Ser Asp Ile Thr Lys Gln Ile Ser Arg Asp Tyr Gly Val Leu
388                     165                     170                     175
391 Leu Glu Ser Ala Gly Ile Ala Leu Arg Gly Leu Phe Ile Ile Asp Pro
392             180                     185                     190
395 Asn Gly Val Val Lys His Leu Ser Val Asn Asp Leu Pro Val Gly Arg
396             195                     200                     205
399 Ser Val Glu Glu Thr Leu Arg Leu Val Lys Ala Phe Gln Phe Val Glu
400         210                     215                     220
403 Thr His Gly Glu Val Cys Pro Ala Asn Trp Thr Pro Glu Ser Pro Thr
404 225                     230                     235                     240
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408                     245                     250                     255
411 Gln
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435 <400> SEQUENCE: 8
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440 <211> LENGTH: 28
441 <212> TYPE: DNA
442 <213> ORGANISM: Artificial Sequence
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VERIFICATION SUMMARY   DATE: 08/29/2005
PATENT APPLICATION: US/10/642,272A   TIME: 17:51:17

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